

# SCORE Search Results Details for Application 09961086 and Search Result 20080917\_142911\_us-09-961-086a-1.rpr.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
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This page gives you Search Results detail for the Application 09961086 and Search Result 20080917\_142911\_us-09-961-086a-1.rpr.

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GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: September 18, 2008, 22:00:18 ; Search time 41 Seconds  
(without alignments)  
1537.121 Million cell updates/sec

Title: US-09-961-086A-1  
Perfect score: 3352  
Sequence: 1 MSSSNVEVFIPVSGQNTNGF.....MIVIFLTIAYLKLLFLKKYS 655

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2849.5	85.0	656	2	JC7860	brain multidrug re
2	835.5	24.9	1049	1	S19421	ATP-dependent perm

3	812	24.2	687	1	FYFFW	white protein - fr
4	800.5	23.9	737	2	T46101	ABC transporter-li
5	774	23.1	646	2	C86441	probable ABC trans
6	767.5	22.9	687	2	D96553	hypothetical prote
7	746	22.3	649	2	A84509	probable ABC trans
8	745	22.2	725	2	T47652	ABC transporter-li
9	741.5	22.1	739	2	T45891	ABC transporter-li
10	739	22.0	678	2	H96552	hypothetical prote
11	726.5	21.7	708	2	T47650	ABC transporter-li
12	721	21.5	635	2	T08934	hypothetical prote
13	720.5	21.5	755	2	G84791	probable ABC trans
14	717.5	21.4	740	1	T02567	probable ATP-bind
15	712.5	21.3	609	2	E96742	probable ABC trans
16	710	21.2	638	2	G02068	white homolog - hu
17	708	21.1	646	2	JC7777	ATP binding casset
18	707.5	21.1	547	2	T31543	hypothetical prote
19	707.5	21.1	720	2	T47648	ABC transporter-li
20	677	20.2	559	2	B88474	protein C05D10.3 [
21	676	20.2	725	2	C84423	probable ABC trans
22	669	20.0	659	2	E86313	hypothetical prote
23	664	19.8	608	2	T34391	hypothetical prote
24	660	19.7	662	2	T47649	ABC transporter-li
25	658.5	19.6	1294	2	S77690	probable membrane
26	657.5	19.6	1450	2	T45888	ABC transporter-li
27	656.5	19.6	590	2	B96573	protein F12M16.17
28	649.5	19.4	633	2	T19189	hypothetical prote
29	645.5	19.3	577	2	T04229	ABC-type transport
30	639	19.1	658	2	T31958	hypothetical prote
31	636.5	19.0	639	2	G88839	protein C10C6.5 [i
32	636.5	19.0	695	2	T21109	hypothetical prote
33	627.5	18.7	610	2	T19333	hypothetical prote
34	612.5	18.3	1501	2	S50992	SNQ2 protein - yea
35	612	18.3	1530	2	S52239	brefeldin a resist
36	603	18.0	1530	2	T52010	hypothetical prote
37	602	18.0	1511	2	A53151	pleiotropic drug r
38	594	17.7	1564	2	S55517	probable transport
39	593	17.7	1443	2	T02491	probable ABC trans
40	590	17.6	1469	2	H96622	probable ABC trans
41	585	17.5	1333	2	S63403	probable membrane
42	580.5	17.3	1420	2	T02644	ABC-type transport
43	580.5	17.3	1529	2	S69688	hypothetical prote
44	572	17.1	1413	2	G84790	probable ABC trans
45	564	16.8	1466	2	T30566	ATP-binding casset

## ALIGNMENTS

## RESULT 1

JC7860  
 brain multidrug resistance protein, BMDP - pig  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 18-Nov-2002 #sequence\_revision 18-Nov-2002 #text\_change 09-Jul-2004  
 C;Accession: JC7860  
 R;Eisenblaetter, T.; Galla, H.J.  
 Biochem. Biophys. Res. Commun. 293, 1273-1278, 2002  
 A;Title: A new multidrug resistance protein at the blood-brain barrier.

A;Reference number: JC7860; MUID:22050127; PMID:12054514  
 A;Accession: JC7860  
 A;Molecule type: mRNA  
 A;Residues: 1-656 <EIS>  
 A;Cross-references: UNIPROT:Q8MIB3; UNIPARC:UPI0000087EC5; GB:AJ420927  
 A;Experimental source: brain  
 C;Comment: This protein, a new transport protein of the ATP-binding cassette (ABC) superfamily of transporters, expressed in porcine brain capillary endothelial cells, plays an important role in the exclusion of xenobiotics from the brain and participates in drug transport across the blood-brain barrier and therefore is considered as a efflux pump at the cerebral endothelium.  
 C;Genetics:  
 A;Gene: bmdp

Query Match 85.0%; Score 2849.5; DB 2; Length 656;  
 Best Local Similarity 84.3%; Pred. No. 2.7e-192;  
 Matches 553; Conservative 44; Mismatches 58; Indels 1; Gaps 1;

Qy	1	MSSSNVEVFI	PVSQNGNTNG	FPATASNDL	KAFTEGAVLS	FNHCINCYR	VKLKSGFL	PCRK	PKPVE	60
		:::	::		::		::			
Db	1	MSSNSYQVS	IPMSKRNTNG	LPGSSSNEL	KTSAGGAVLS	SFHDIC	YRVKVS	SGFL	FCRK	60
Qy	61	KEILSNING	IMKPLNAIL	LGPTGGGK	SSLLDVL	LAARKDP	SGLSGD	VLINGA	PRPAN	120
		::								
Db	61	KEILTNING	IMKPLNAIL	LGPTGGGK	SSLLDVL	LAARKDP	HGLSGD	VLINGA	PRPAN	120
Qy	121	SGYVVQDD	VVMGTLTV	RENQLQF	SAALRLAT	TMTNHEK	NERINR	VIQELG	LDKVAD	180
Db	121	SGYVVQDD	VVMGTLTV	RENQLQF	SAALRLPT	TMTNHEK	NERINM	VIQELG	LDKVAD	180
Qy	181	QFIRGVSG	GERKRTS	SIGMELIT	DPISILFL	DEPTTGL	DSSTANA	VLALLL	KRMSKQ	240
Db	181	QFIRGVSG	GERKRTS	SIAMELIT	DPISILFL	DEPTTGL	DSSTANA	VLALLL	KRMSKQ	240
Qy	241	SIHQPRYS	IFKLFDSL	TLLASGR	LMFHGPA	QEALGYF	ESAGYH	CEAYNN	PADFFLD	300
Db	241	SIHQPRYS	IFKLFDSL	TLLASGR	LMFHGPARE	ALGYFAS	IGYNCE	PYPNNP	ADFFLD	300
Qy	301	DSTAVALNR	-EEDFKATE	IIIEPSKQ	DKPLIEK	LAIEYVN	SSFYKET	KAEHLQ	LSGGEK	359
		::	::	::	::	::	::	::	::	
Db	301	DSSAVVLS	RRADRDE	GAQEPEPE	PEKDTPL	IDKLA	AFYTN	SSFFK	DKTKVEL	360
Qy	360	KITVFKEIS	YTTSFCH	QLRWVSK	RSFKNLL	GNPQASIA	QIIIVTV	VVLGLV	IGAIYF	419
		::	::	::	::	::	::	::	::	
Db	361	KSSVYKEV	TYTTSFCH	QLRWISRR	SFKNLLG	NPQASVA	QIIIVTI	ILGLVIG	IAIFYD	420
Qy	420	STGIQNRA	GVLFLLT	TNQCFSS	VSVAVEL	FVVEKK	LFIEH	YISGYR	VSSYFL	479
		::								
Db	421	PSGIQNRA	GVLFLLT	TNQCFSS	VSVAVEL	LVVEKK	LFIEH	YISGYR	VSSYFF	480
Qy	480	PMTMLPSI	IIFTCIVY	FMLGLK	PKADAF	VMMF	TLMVAYS	SASSMA	LAIAAG	539
				::	::	::				
Db	481	PMRMLPSI	IIFTCITY	FLGLK	PAVG	SFFIM	MTLMVAYS	SASSMA	LAIAAG	540
Qy	540	LMTICFV	FMFMIF	SGLLVN	LNTTIAS	WLSWLQ	YFSIPR	YGF	TALQHNE	599
Db	541	LMTISFV	FMFMIF	SGLLVN	LKTVVP	WLSWLQ	YFSIPR	YGF	SALQYNE	600

S19421  
ATP-dependent permease ADP1 precursor - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: protein YCR011c; protein YCR105  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: S19421; S40914  
R;Goffeau, A.; Purnelle, B.; Skala, J.  
submitted to the Protein Sequence Database, March 1992  
A;Reference number: S19420

A;Accession: S19421  
A;Molecule type: DNA  
A;Residues: 1-1049 <GOF>  
A;Cross-references: UNIPROT:P25371; UNIPARC:UPI00001255FD; EMBL:X59720; NID:g1907116; PIDN:CAA42328.1; PID:g1907154; GSPDB:GN00003; MIPS:YCR011c  
R:Purnelle, B.; Skala, J.; Goffeau, A.

A;Title: The product of the YCR105 gene located on the chromosome III from *Saccharomyces cerevisiae* presents homologies to ATP-dependent permeases.

A;Accession: S40914  
A;Status: not compared with conceptual translation

A;Residues: 1-1049 <PUR>  
A;Cross-references: UNIPARC:UPI00001255FD

Yeast 8, 409-417, 1992

A;Title: The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of chromosome III from *Saccharomyces cerevisiae* reveals seven open reading frames including the RVS161, ADP1 and PGK genes.

A;Contents: annotation

A:Gene: SGD:ADP1: MIPS:YCR011c

A;Cross-references: SGD:S0000604; MIPS:YCR011c

C;Superfamily: ATP-dependent permease ADP1; ATP-binding cassette homology  
C;Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein  
F:1-25/Domain: signal sequence #status predicted <SIG>

F;26-1049/Product: ATP-dependent permease ADP1 #status predicted <MAT>

F:26-324/Domain: extracellular #status predicted <EXT>

F:325-341/Domain: transmembrane #status predicted <TM1>

F:406-607/Domain: ATP-binding cassette homology <ABC>

F:423-430/Region: nucleotide-binding motif A (P-loop)

F:550-557/Region: nucleotide-binding motif B

F:794-810/Domain: transmembrane #status predicted <TM2>

F:829-845/Domain: transmembrane #status predicted <TM3>

F:878-894/Domain: transmembrane #status predicted <TM4>

F:909-925/Domain: transmembrane #status predicted <TM5>

F:938-954/Domain: transmembrane #status predicted <TM6>

F:1025-1041/Domain: transmembrane #status predicted <TM7>

F;50,114,165,221/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;429/Binding site: ATP (Lys) #status predicted

Query Match 24.9%; Score 835.5; DB 1; Length 1049;  
 Best Local Similarity 30.5%; Pred. No. 1.8e-50;  
 Matches 222; Conservative 134; Mismatches 257; Indels 115; Gaps 18;

```

Qy      1  MSSSNVEVFIPIVQSGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      355 LGSSKSPIRLP-DEDAVNNFLQNEDDL-----ATLSFENITYSVPSINS-----DGVE 402

Qy      61  KEILSNINGIMKPG-LNAILGPTGGGKSSLLDVLAAARKDPSGLSGDVLINGAPRP-ANFK 118
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      403 ETVLNEISGIVKPGQLAIMGGSGAGKTLLDILAMKRRTGHVSGSIKVNIGISMDRKSFS 462

Qy      119  CNSGYVVQDDVVMGTLTVRENLFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKV 178
      | : | | | : : | | | : | | | : : | : | : | : | : | : |
Db      463 KIIGFVDQDFLLPTLTVFETVLNSALLRLPKALSFEAKKARVYKVEELRIIDIKDRII 522

Qy      179  GTQFIRGVS GGERKRTSIGMELITDPSILFLDEPTTGLDSSSTANAVLLLLKRMKSQ-GRT 237
      : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      523 GNEPDRGISGGEKRRVSIACELVTSPLVLFLDEPTSGLDASANNVIECLVRLSSDYNRT 582

Qy      238  IIFSIIHQPRYSIFKFLDSLTLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDI 297
      : : | | | | : | | | : | : | : | : | : | : | : | : | : |
Db      583 LVLISIHQPRSNIFYLPDKLVLLSKGEMVYSGNAKKVSEFLRNEGICYDPNYNIADYLIDI 642

Qy      298  -----INGDSTAV 305
      : |
Db      643 TFEAGPGQKRRIRNISDLEAGTDTNDIDNTIHTTFTSSDGTQREWAHLAAHRDEIRS 702

Qy      306  ALNREEDFKATE----IIEPSKQDKPLIEKLAEIYVNSSPFYKETKAELHQ-LSGGEKKKK 360
      | | | : : | : | : | : | : | : | : | : | : | : | : |
Db      703 LLRDEEDVEGTGRRGATEIDLNTKLLHDK----YKDSVYVYAEALSQEIIEVLSEGDEESN 758

Qy      361  IT--VFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKN 418
      : : | : | : : | | | : | : : : | : | : | : | : | : |
Db      759 VLNGLDPTGQQSAGFLQQLSILNSRSFKNMYRNPKLLGNLYLLTILLSLFLGTLYYNVSN 818

Qy      419  DSTGIQNRAGVLFLLTITNQCFSSVASVELFVVEKKLFIHEYISGYRVSFYFLGKLLSDL 478
      | : | | : | : | : : : | : : | : | : | : | : | : | : |
Db      819 DISGFQNRMGLEFFILTIFYGFVTFITGLSSFALERIIFIKERSNNYISPLAYYISKIMSEV 878

Qy      479  LPMTMLPSIIFTCIVFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVAT 538
      : : : : | : : | | | : | : | : | : | : | : | : | : |
Db      879 VPLRVVPPILLSLIVPMTGLNMKDNAFFKICIGILILFNGLGISLEILTIGIIFEDLNNSI 938

Qy      539  LLMTICVFMMIFSGLLV---NLTTIASWLSWLQYFSIPRYGFTALQHNEF----- 586
      : | : : : | | | : | : | : | : | : | : | : | : | : |
Db      939 ILSVLVLLGSLLEFSGLFINTKNITNVA--FKYLNKFSVFYYAYESLLINEVKTLMLKERK 996

Qy      587  LGQNF-CPGLNATGNPNPCNYATCTGEEYLVKQGI--DLSPWGLWNKHVALACMIVIFLTI 643
      | | | : | | : | : | : | : | : | : | : | : | : | : |
Db      997 YGLNIEVPG-----ATILSTFGFVVQNLVFDIK-----ILALFNVVVFLIM 1036

Qy      644  AYLKLLFL 651
      | | : :

```

Db 1037 GYLALKWI 1044

RESULT 3

YFFFW

white protein - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 31-Dec-1990 #sequence\_revision 17-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S08635; S07263; S10240

R;Pepling, M.; Mount, S.M.

Nucleic Acids Res. 18, 1633, 1990

A;Title: Sequence of a cDNA from the *Drosophila melanogaster* white gene.

A;Reference number: S08635; MUID:90221897; PMID:2109311

A;Accession: S08635

A;Molecule type: mRNA

A;Residues: 1-687 <PEP>

A;Cross-references: UNIPROT:PI0090; UNIPARC:UPI000011F0A1; EMBL:X51749; NID:g8825; PIDN:CAA36038.1; PID:g8826

R;O'Hare, K.; Murphy, C.; Levis, R.; Rubin, G.M.

J. Mol. Biol. 180, 437-455, 1984

A;Title: DNA sequence of the white locus of *Drosophila melanogaster*.

A;Reference number: S07263; MUID:85134865; PMID:6084717

A;Accession: S07263

A;Molecule type: DNA

A;Residues: 1-24, 'LIFEIPYHCRVTAD', 30-

334, 'ITLHLNSYPAPWPSVLPTTIRRTFTYRCWPLCPDGRSSPVIGSPRYG', 372-687 <OHA1>

A;Cross-references: UNIPARC:UPI000016B571; EMBL:X02974

A;Experimental source: strain Canton S

R;O'Hare, K.

submitted to the EMBL Data Library, June 1985

A;Reference number: S10240

A;Accession: S10240

A;Molecule type: DNA

A;Residues: 1-24, 'LIFEIPYHCRVTAD', 30-687 <OHA2>

A;Cross-references: UNIPARC:UPI000016BDF; EMBL:X02974; NID:g10873; PIDN:CAA26716.1; PID:g10874

A;Experimental source: strain Canton S

C;Genetics:

A;Gene: white; w

A;Cross-references: FlyBase:FBgn0003996

A;Introns: 24/3; 116/1; 334/2; 439/3; 483/3

C;Superfamily: fruit fly white protein; ATP-binding cassette homology

C;Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein

F;113-317/Domain: ATP-binding cassette homology <ABC>

F;130-137/Region: nucleotide-binding motif A (P-loop)

F;261-265/Region: nucleotide-binding motif B

F;67,93,472,554,651/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.2%; Score 812; DB 1; Length 687;

Best Local Similarity 32.1%; Pred. No. 4.4e-49;

Matches 210; Conservative 134; Mismatches 251; Indels 60; Gaps 17;

Qy 5 NVEVFIPVSGNTNGFPATASNDLKAFTEGAVLSFHNICRYVKLKSGLFPCRPKPEKEIL 64  
|:::| |:| | : | | | : :| | : |::|

Db 74 NMDIFGAVNQ-----PGSGWRQLVNRTRGLFCNERHI-----PAPR---KHLL 113

Qy 65 SNINGIMKPG-LNAILGPTGGGKSSLLDVLAARKDPSGL----SGDVLINGAPRPA-NFK 118

Db	114	KNVCGVAYPPELLAVMGSSGAGKTTLLNALAFR-SPQGIQVSPSGMRLNLNQPVDAKEMQ	172
Qy	119	CNSGYVVQDDVVMGTLTVRENLFQSAALRLATTMTNHEKNERINRVIQELGLDKVADSKV	178
Db	173	ARCAYVQDDLFIGSLTAREHLIFQAMVRMRHLTYRQVRARVDQVIQELSLSKCQHTII	232
Qy	179	GTQ-FIRGVSGGGERKRTSIGMELITDPSILFLDEPTTGLDSSATANVLLLKRMKSQGR	237
Db	233	GVPGRVKGLSGGERKRLAFASEALTDPELLICDEPTSGLDSTAHSVVQVLKKLKSKQKGT	292
Qy	238	IIFSIIHQPRYSIFKLFDSLTLASGRMLFHGPAQEALGYFESAGYHCEAYNNPADFFLDI	297
Db	293	VILTIHQPSSELFELFDKILLMAEGRVAFLGTPSEAVDFFSYVGAQCPTNYPADFYVQV	352
Qy	298	INGDSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETAKELHLQSGGEK	357
Db	353	L-----AVVPGREIESR-----DRIAKICDNFAISKVAR-DMEQLLATKN	391
Qy	358	KKKITVFKEISYT--TSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFG	415
Db	392	LEKPLEQPPENGYIKATWFMQFRAVLWRSWLSVLKEPLLVKRLIQTMTMVAIIIGLIFLG	451
Qy	416	LKNDSTGIQNRAGVLFLLTTNQCFSSVSA-VELFVVEKKLFIHEYISGYYRVSSYFLGKL	474
Db	452	QQLTQVGVMNINGAIFLFLTNMTFQNVFATINVFETSELPVFMREARSRLRYCDTYFLGKT	511
Qy	475	LSDLLPMTMLPSIIFTICIVYFMLGLPKADAFVMMFTLMMVAYSASSMALAIIAAGQSVV	534
Db	512	IAE-LPLFLTVPVLVFTAIAYPMIGLRAGVLHFFNCLALVTLVANVSTSGYLISCASSST	570
Qy	535	SVATLLMTICFVFMFIFSGLLVNLTTIASWSLWQYFSIPRYGFTALQHNEFLGQNFQCPG	594
Db	571	SMALSVGPPIVIFFLLFQGGFFLNSGSPVYLVKLSYLSWFRYANEGLLINQWADVE--PG	628
Qy	595	-LNATGNPNPNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKL	648
Db	629	EISCTSSN---TTCPSGGKIVLETLNFSADPLDYVGLAILVYSFRVLAYLAL	679

#### RESULT 4

T46101  
ABC transporter-like protein - *Arabidopsis thaliana*  
N;Alternate names: protein T25B15.80  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C;Accession: T46101  
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.  
X.; Quetier, F.; Salanoubat, M.  
submitted to the Protein Sequence Database, January 2000  
A;Reference number: Z23021  
A;Accession: T46101  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-737 <ALC>  
A;Cross-references: UNIPROT:Q9FT51; UNIPARC:UPI00000A69DB; EMBL:AL132972  
A;Experimental source: cultivar Columbia; BAC clone T25B15

C;Genetics:

A;Map position: 3

A;Introns: 122/1; 146/3; 225/2; 277/2; 338/3; 422/2; 535/1; 628/3; 664/3

A;Note: T25B15.80

Query Match 23.9%; Score 800.5; DB 2; Length 737;  
 Best Local Similarity 31.4%; Pred. No. 3.1e-48;  
 Matches 211; Conservative 132; Mismatches 227; Indels 101; Gaps 21;

```

Qy      27 DLKAFTEGAV-----LSFHNICYRVKLKSGFLPCRKPVEKEILSNNINGIMKPG-  74
      |:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      124 DIEAATSSVVKFQAEPTFPIYLKFIDITYKVTTKG----MTSSSEKSLNGISGSAYPGE  179

Qy      75 LNAILGPTGGKSSLLDVLAAKRDPSGLSGDVLINGAPRPANFKCNSGYVVQDDVVMGTL  134
      |:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      180 LLALMGPSGSGKTTLLNALGGRFNQQNIGGSVSYNDKPYSKHLKTRIGFVTDQDVLFPHL  239

Qy     135 TVRENLFQSAALRLATTMINHEKNERINRVIQELGLDKVADSKVGTFQIRGVSGGERKRT  194
      |:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     240 TVKETLTYTALLRLPKTLTEQEKEQRAASVQIELGLERCQDMMIGGSFVRGVSGGERKRV  299

Qy     195 SIGMELITDPSILFLDEPTTGLDSSSTANAVLLLLKRMSKQGRTIIFSIIHQPRYSIFKLFED  254
      |:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     300 CIGNEIMTNPSSLLLDDEPTSSLDSTALKIVQMLHCIAKAGKTIVTTIHQPSSRLFHRFD  359

Qy     255 SLTLLASGRMLFHGPAQEALGYFESAGYHCEAYNNPADFFLDIINGDSTAVALNREEDFK  314
      |:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     360 KLVVLSRGSLLYFGKASEAMSYFSSIGCSPLLAMNPAEFLDLVNGNMNDIS-----  411

Qy     315 ATEIIIEPSKQDKPLIEKLAEIYVNS-----SFYKETKAELHQLS-----GGE  356
      : : : | | : | | : | | : | | : | | : | | : | | : | | : |
Db     412 ---VPSALKEKMKIIRL-ELYVRNVKCDVETQYLEEAYKTIQIAVMEKMKLMAPVPLDEE  466

Qy     357 KKKKITVFKE---ISYTTSCF-HQLRWVSKRS---FKNLLGNPQASIAQIIVTVVLGLVI  409
      | | | | | : | | : | | | | | | | | | | | | | | | | | | |
Db     467 VKLMITCPKREWGLSNWEQYCLLSLRGKERRHDYFSWL-----RVTVQLSTAI---IL  517

Qy     410 GAIYFGLKNDSTGIQ-NRAGVLFLLTTNQCFSSV-SAVELFVVEKKLFIHEYISGYRRVS  467
      | : : : | | : | | : | | : | | : | | : | | : | | : | | : |
Db     518 GLLWW---QSDITSQRPTRSGLLFFIAVFWGFFPVFTAIFTFPQERAMLSKERESNMYRLS  575

Qy     468 SYFLGKLLSDLLPMTMLPSIIFTICIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAI  527
      : | : : | | | | : : : | : | | | | | | | : | : : | : | | |
Db     576 AYFVARTTSD-LPLDLILPVLFLVVVYFMAGLRLRAESFFLSVLTVFLCIVAAQGLGLAI  634

Qy     528 AAGQSVSVSATLLMTICVFMMIFSGLLVNLTIIASWLSWLQYFSPRYGFAL---QHN  584
      | : : | | | : : : | : | | : : : | : : | : : | : : | : |
Db     635 GASLMDLKKATTLASVTVMFMLAGGYFVK--KVPFFIAWIREMSFNHYTKLLVKVQYE  692

Qy     585 EFLGQNFQPLNATGNNPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTI  644
      | : : : : : : | | | : | : | | | | | | | | | | | | | | | |
Db     693 EIM-----ESVNGEE--IESGL-----KEVSALVAMIIGYRLVA  724

Qy     645 YLKLLFLKKYS 655
      | | : | : |
Db     725 YFSLRRMKLHS 735
  
```



<http://es.ScoreAccessWeb/GetItem.action?AppId=099610...7142911-us-09-961-086a-1.mpr&ItemType=4&startByte=0> (9 of 24)/22/2008 12:04:28 PM

```

Qy      332 L-AEI-YVNSSFYKETKAELHQLSGGEKKKITVFKEISYTTSFCHQL-----RWVSKRS 384
      | | | : | : | | | | | : | : | : | : | : |
Db      349 LKAELCNAESHSEYETKAAAKNL-----KSEQWCTTWWYQFTVLQGRVRRER 396

Qy      385 FKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDSTGIQNRAGVLFFLTNNQCFSSV-S 443
      | : : : | | : | | | | : : : | : | : | : | : :
Db      397 FESF---NKLIRIFQVISVAFVG---GLLWW--HTPKSHIQDRTALFFFSVFVWGYPYLYN 448

Qy      444 AVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLLPMTMLPSIIFTCIVYFMLGLKPKA 503
      | | | | : | | | | : | : | : | : | : |
Db      449 AVFTFPQEKRMILIKERSSGMYRLSSYFMARNVGD-LPLELALPTAFVFIYWMGGLKDPD 507

Qy      504 DAFFVMMFTLMMVAYS---ASSMALAIAAGQSVSVSATLLMTICVFMMMFISGLLVNLT 560
      | : : | : | | : | | | : | | : | | : : : |
Db      508 TTF---ILSLLVLYSVLVAQGLGLAFGALLMNIKQATTLASVTTLVFLIAGGYVYQ--Q 562

Qy      561 IASWLSWLQYFSIPRYGFTALQHNEFLGQNFPCPLNATGNNPCNYATCT-----GEEY 613
      | : : | : | | : | | : | : | : | : | :
Db      563 IPPPIVWLKYLSSYSYYCYKLLL-----GIQYTD--DYECESKGVWCRVGDGP 608

Qy      614 LVK-QGIDLSPWGLWKNHVALACMIVIFLTIAYLKL 648
      : | : : | : : : | : : : | : |
Db      609 AIKSMGLN---NLWIDVFVMGVMLVGYRLMAYMAL 640

```

## RESULT 6

D96553

hypothetical protein F5D21.6 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: D96553

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C. Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, A.; Militischer, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L. J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D96553

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-687 &lt;STO&gt;

A:Cross-references: UNIPROT:Q9C8K2; UNIPARC:UPI00000AB8E7; GB:AE005173; NID:g10092349; PIDN: AAG12758.1; GSPDB:GN00141

C:Genetics:

A:Gene: F5D21.6

A:Map position: 1

C;Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-binding cassette homology

Query Match	22.9%;	Score 767.5;	DB 2;	Length 687;
Best Local Similarity	32.6%;	Pred. No. 5.9e-46;		
Matches 212;	Conservative 118;	Mismatches 244;	Indels 77;	Gaps 21;
Qy	34	GAVLSFHNNICRVKLSGFLPCRKPVEKEILSNINGIMKPG-LNAILGPTGGGKSSLLDV	92	
Db	21	GAYLAWEDLTVVIPNFGSGG-PTRR-----LLDGLNGHAEPRGIMAIMGSPSGSKSTLLDS	74	
Qy	93	LAARKDSPG-LSGDVLINGAPRPANFKCNSGYVQDDVVMGTLTVRENLQFSAALRLATT	151	
Db	75	LAGRLARNVIMTGNLLNGKKARLDYGL-VAYVTQEDILMGTLTVRETTITYSAHLRLSSD	133	
Qy	152	MTNHEKNERINRVIQELGLDKVADSKVGTQFIRGVSGGERKRTSIGMELITDPSILFLDE	211	
Db	134	LTKEEVNDIVEGTIIELGLQDCADRVIGNWHSRGVSGGERKRVSALEILTRPQILFLDE	193	
Qy	212	PTTGLDSSTANAVLLLLKRMKSQ-GRTIIFSIHQPRYSIFKLFDSLTLASGRMLMFHGA	270	
Db	194	PTSGLDASAFFVIQALRNRIARDGGRTVVSSIHQPSSEVPALFDDLFLSSGETVYFGES	253	
Qy	271	QEALGYFESAGYHCEAYNNPADFFLDIINGDSTAVALNREEDFKATEIIEPSKQDKPLIE	330	
Db	254	KFAVEFFAEAGFPCKKRNPSDHFLRCINSDFDVTATLKGSQLRIRE--TPATSD-PLMN	310	
Qy	331	-----KLAIEIYVNSSFYKETKAEHLQLSGGE-----KKKKITVFKEISYTTSF	374	
Db	311	LATSEIKARLVENYRRSVYAKSAKSRIRELASIEGHGMEVVRKGSSEATWFK-----	361	
Qy	375	HQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGAIYFGLKNDSTGIQNRAGVLFFLT	434	
Db	362	-QLRTLTKRSFVNMCRDIGYYWSRIVYIVVSFVCGVTIFYDVGHYSITSILARVSCGGFIT	420	
Qy	435	TNQCFSSVSVALELVVEKKLFIHEYISGYRVSSYFLGKLLSDLLPMTMLPSIIFTTCIVY	494	
Db	421	GFMTFMSIGGFPFIEEMKVIFYKERLSGGYGVSVYIIISNVSS-FPFLVAIALITGSITY	479	
Qy	495	FMLGLKPKAD--AFF-----VMMFTLMMVAYSASSMALAIAAGQSVSVSATLLMTI	543	
Db	480	NMVKFRPGVSHWAFFCLNIFFSVSVIESLMMVVASLVPNFMGLITGAGIIGI--IMM	537	
Qy	544	CFVFMFISGLLVNLTITIASWLSWLQYFSIPRYGFTALQ---HNEFLGQNFPCPLNATGN	600	
Db	538	GFF-----RLLPDLPKV----FWRYPIFSMSYGSWAIQYAGYKNDPLGLEFDPMF----	582	
Qy	601	NPCNYATCTGEEYLVK-QGIDLSP---WGLWKNHVALACMIVIFLTITAYLK	647	
Db	583	--AGEPKMTGEQVINKIFGVQVTHSKWDLAIVLILVCYRILFFIVLKLK	631	

RESULT 7

A84509

probable ABC transporter [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004







```

Db      87 VLSFKDLTVSYVKIKKKFKFPCCGNSPFDGNDMEMNTKVLNGLISGEAREGEMMAVLGAS 146

Qy      83 GGGKSSLLDLVAARKDPSGLSGDVLINGAPRPANF-KCNSGYVQDDVVMGTLTVRENLO 141
      | |||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     147 GSGKSTLIDALANRISKESLRGDITLNGEVLESSLHKVISAYVMQDDLLFPLMTVEETLM 206

Qy     142 FSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGTQFIRGVSGGERKRTSIGMELI 201
      ||| || :::: :| :| :| :||| | : :| : | | | | | | | | | | | |
Db     207 FSAEFLRPLSSSKKKKKARVQALIDQLGLRNAAKTVIGDEGHRGVSGGERRRVSIGTDII 266

Qy     202 TDPISILFDEPTTGLDSSTANAVLLLLKRMKQGRITIFSHPQRYISFKLFDLSLTLLAS 261
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     267 HDPIILFDEPTSGLDSTAYMVVKVLQRIAQSGSIVIMSIHQFSYRILGLDLKLIFLSR 326

Qy     262 GRIMFHGPAQALGYFESAGYHCEAYNNPADFFLDIINGDSTAVALNREEDFKATEIIEP 321
      | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     327 GNTVYSGSPHLPQFFSEFGHIPENENKPEFALDLIR-----ELED 369

Qy     322 SKQDKPLIEKLAEIYVNSSFFYKETAELHQLSGGEKKKKITVFKEI----- 367
      : | | : | | : | : | : | : | : | : | : | : | : | : | : | : |
Db     370 PEGTKSLVE-----FHQWRK--QTSSQSRRTNVSLKDAISASISRGKLVSGA 417

Qy     368 -----SYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKND 419
      : : | : : : | | | | | | : : : : | | : : | : : | : : | : |
Db     418 TNLRSSQTFANPFWTEMLVIGKRSILNSRRQPELFGIRLGAVLVTGMILATIFWKLDNS 477

Qy     420 STGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRYVSSYFLGKLLSDLL 479
      ||| | | | : : : | : : | : : | : : | : | | | | : : :
Db     478 PRGIQERLGFFAFAMSTTFYTCAEAIPVFLQERYIFMRETAYNAYRRSSVLAHTIIS-I 536

Qy     480 PMTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAGQSVSVSATL 539
      : : | : : : : | : : | : | : : | : : | : : | : | : | : |
Db     537 PALIILSAAFAASTFSAVGLAGGSEGLFFFTILTAFWAGSSFVTFSLGVVSHVMIGFT 596

Qy     540 LMTICVFVMMIFSGLLVNLTTIASWLSWLQYFISIPRYGFTALQHNEFLGQNFC---PGLNA 597
      : : : : | | : : | : | : | : | : | : | : | : | : | : |
Db     597 VVVAILAYFLFLSFGFFISRDRIPLYWIFHYLSLVKYPYEGVLQNEFEDPTKCFVRGIQM 656

Qy     598 TGNNPCNYA-----TC--TGEEYLVKQGI-DLSPWG-LWKNH 630
      : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     657 FDN SPLQVPTAVKISLLKSMGVLGINVTAETCVTTGIDILKQQGITEISKWNCLW--- 713

Qy     631 VALACMIVIFLTIA---YLKLLF 650
      : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db     714 -----ITVAGGFFFRVLV 726

```

## RESULT 10

H96552

hypothetical protein F5D21.8 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: H96552

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.

[http://es.ScoreAccessWeb/GetItem.action?AppId=099610...7\\_142911\\_us-09-961-086a-1.rpr&ItemType=4&startByte=0](http://es.ScoreAccessWeb/GetItem.action?AppId=099610...7_142911_us-09-961-086a-1.rpr&ItemType=4&startByte=0) (16 of 24)9/22/2008 12:04:28 PM



```

| : | : | | | : | : : | : : | | | : : |
Db 444 YGVAVYIVTSNLLSS-LPFIILMCLSTSSITIIYMRVFSQSGSHFFYNCLDLICAITTVESC 502

Qy 524 ALAIAAGQSVSVSATLLMTIC----FVFMFISGLLVNLTIIASWLSWLQYFISIPRYGFT 579
: ||: | | : | : : | : | : | | |
Db 503 MMMIAS-----VVPNFLMGVLMGAGYIGIMVLSAGFFRFFPDLPWVFWRYPVSYINYGAW 557

Qy 580 ALQ---HNEFLGQNFPCPLNATGNNPCNYATCTGEEYLVKQIDLSPWGLWKNHVALACM 636
||| | | : | : : | : | : : | : |
Db 558 ALQGAYKNEMIGVEY-----DSPLPLVPKMKGELILQTVLGINPESSKWLDLAVVMM 609

Qy 637 IVIFLTIAYLKLL 649
| : | | : : |
Db 610 ILIGYRIAFFAIL 622

```

## RESULT 11

T47650

ABC transporter-like protein - Arabidopsis thaliana

N;Alternate names: protein T15C9.110

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C;Accession: T47650

R;Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.

submitted to the Protein Sequence Database, April 2000

A;Reference number: Z24470

A;Accession: T47650

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-708 &lt;MEW&gt;

A;Cross-references: UNIPROT:Q9M2V5; UNIPARC:UPI00000A627B; EMBL:AL132970

A;Experimental source: cultivar Columbia; BAC clone T15C9

C;Genetics:

A;Map position: 3

A;Note: T15C9.110

C;Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-binding cassette homology

```

Query Match          21.7%; Score 726.5; DB 2; Length 708;
Best Local Similarity 30.1%; Pred. No. 4.7e-43;
Matches 198; Conservative 123; Mismatches 282; Indels 55; Gaps 15;

```

```

Qy 36 VLSFHNICRYRVKLKSGFLPCRKPVE--KEILSNINGIMKPG-LNAILGPTGGGKSSLLDV 92
| | | : | | : | : | : | : | : | : | : | : | : |
Db 62 LLSFNNLISYNNVLRRRFDFSRKKTASVKTLLDDITGEARDGEILAVLGGSGAGKSTLIDA 121

Qy 93 LAARKDPSGLSGDVLINGAP--RPANFKCNSGYVQDDVVMGTLTVRENLFQSAALRLAT 150
| | | | | | : | | : | | : | : | : | : | : | : |
Db 122 LAGRVAEDSLKGTVLINGEKVLQSRLKVISAYVMQDLLFPMLTVKETLMFASEFRLEPR 181

Qy 151 TMTNHEKNERINRVIQELGLDKVADSKVGTQFIRGVSGGERKRTSIGMELITDPSILFLD 210
: : : | | : | : | | | : | : | | | | | | | | | | |
Db 182 SLPSKSKMERVETLIDQLGLRNAADTVIGDEGHRGVSGGERRRVSIGIDIHDPILLFLD 241

Qy 211 EPTTGLDSSTANAVLLLLKRMSKQGRTIIFSIHQPRYSIFKLFDSLTLASGRLMFHGPA 270
| | : | | : | : : | | : | : | | | | | | | | | |
Db 242 EPTSGLDSTNAFMVQVLKRIAQSGSVVIMSIHQPSARIIGLLDRLIILSHGKSVFNGSP 301

```



```

Db      1 MDNQEVSMVDVETPIAKTNDRLPFSIFKKANNPVTLKFENLVYTVKLLKDSQGCGFKNDK 60
      | : | : | : | | : : | | | : | | | | | | | |
Qy      58 PVEKEILSNINGIMKPG-LNAILGPTGGGKSSLLDVLAAAR--KDPGSLSGDVLINGAPRP 114
      | : | | : | : | | : | : | | | | | | : | : | : | |
Db      61 TEERTILKGLTGIVKPGEILAMLGPSGSGKTSLLTAGLGRVGEKGKLTGNISYNNKPLS 120
      | : | : | | : | | | | | : | | : | : | : | : | : |
Qy      115 ANFKCNSGYVQDDVVMGTLTVRENLFQSAALRLATMTNHEKNERINRVIQELGLDKVA 174
      | : | : | | : | | | | | : | | : | : | : | : | : |
Db      121 KAVKRTTGFTVQDDALYPNLTVTETLVFTALLRLPNSFKKQEKIKQAKAVMTELGDRCK 180
      | : | : | | : | | | | | : | : | : | : | : | : | :
Qy      175 DSKVGTQFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSSTANAVLLLLKRMKQ 234
      | : : | | : | | | | | | | | | : : | : | : | : | :
Db      181 DTIIGGFLRGVSGGERKRVSIGQEILINPSLFLDEPTTGLDSTTAQRVSIWLWELARG 240
      | : | : | | | | : | : | : | : | : | : | : | : |
Qy      235 GRTIIFSIHQPRYSIFKFLDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYN-NPADF 293
      | | : : | | | : | : | : | : | : | : | : | : |
Db      241 GRTVVTIHHQP-----SKGNPVYFGLGSNAMDYFASVGYSPVERINPDSF 286
      | | : | | | : | : | : | : | : | : | : | : |
Qy      294 FLDIINGDSTAVALNREEDFKATEIIEPSKQDKPLIEKLAIEIVNSSFYK-----E 344
      | | | | | : : : | : | : | : | : | : | : | : |
Db      287 LLDIANGKPLLV-----ISCWPSVGSDESQRPEAMKAALV----AFYKTNLLDSVINE 335
      | : | : | : : : | : | : | : | : | : | : | : |
Qy      345 TKAELHQLSGGEKKKITVFKEISYTSFCHQLRWVSKRSFKNLLGNPQA--SIAQIIVT 402
      | : : : : : : : | : | : | : | : | : | : | : |
Db      336 VKGQDDLCKNPRESSRVATNTYGDWPTTWWQQFCVLLKRLGKQRHDSFSGMKVAQIF-- 393
      | : | : | : : : | : | : | : | : | : | : | : |
Qy      403 VVLGLVIGAIYFGLKNDSTGIGNRAGVLFLLTNTQCFSSV-SAVELFVVEKKLFIHEYIS 461
      | : | : | : | : | : | : | : | : | : | : | : |
Db      394 -IVSFLCGLLWWQTK--ISRLQDQIGLLFFISSFWAFPLEQQIIFTFQERAMLQKERSS 450
      | : | : | : | : | : | : | : | : | : | : | : |
Qy      462 GYYRVSSYFLGKLLSDLLPMTMLPSIIFTCIVYFMLGLKPKADAFVMMFTLMMVAYSAS 521
      | | | : | | : | | | : | : | : | : | : | : | :
Db      451 GMYRLSPYFLSRVVGDLPEMELILPTCFLVITYWMAGLNHNLANFFVTLVLLVHVLVSG 509
      | | | : | | : | | | : | : | : | : | : | : | :
Qy      522 SMALAIAGQSVSVSATLLMTICVFMMIFSGLLVNLTIASWLSWLQYFSIPRYGFTAL 581
      : | : | | | : | : : : : | : : : | : | : | : |
Db      510 GLGLALGALVMDQKSATTLGVSIMLTFLLAGGYVQHVVPV--FISWIKYVSIQYTYKLL 567
      | : | : | : | : | : | : | : | : | : | : | : |
Qy      582 QHNEFLGQNFQCPGLNATGNN---PCNYATCTGEEYL-VKQGIDLSWPGLWNHVALACMI 637
      | | | : | : | : | : | : | : | : | : | : | :
Db      568 ----ILQYATANELYPCGNGKLRCHVGDGFEKIGHFNSGL-----VSALALTAML 615
      | : | : | : | : | : | : | : | : | : | : | : |
Qy      638 VIFLTIAYLKLFLK 653
      | : | : | : | : |
Db      616 VVYRVIAIYIALTRIGK 631

```

## RESULT 13

G84791

probable ABC transporter [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: G84791

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.;  
 Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.;



<http://es.ScoreAccessWeb/GetItem.action?AppId=099610...7> [4291] us-09-961-086a-1.mpr&ItemType=4&startByte=0 (21 of 24)9/22/2008 12:04:28 PM

A;Residues: 1-740 &lt;STO&gt;

A;Cross-references: UNIPARC:UPI00000AC233; GB:AE002093; NID:g3402672; PIDN:AAC28975.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g39350; T16B24.1; F12L6.1

A;Map position: 2

C;Superfamily: Arabidopsis thaliana probable ATP-binding cassette protein F12L6.1; ATP-binding cassette homology

C;Keywords: ATP

F;110-310/Domain: ATP-binding cassette homology &lt;ABC&gt;

Query Match 21.4%; Score 717.5; DB 1; Length 740;  
 Best Local Similarity 28.0%; Pred. No. 2.1e-42;  
 Matches 193; Conservative 120; Mismatches 294; Indels 83; Gaps 16;

```

Qy      26  NDLKAFTEGAVLSFHNICYRVKLK-----SGFLPCR-----KPVEKEILSNING 69
      || | | ||| | : | : | | | | : | | : | : | |
Db      56  NDGYMRTVPFVLSFDNLTYNVSVRPKLDFRNLFPRRRTDEPIAQTARPKTKTLNNISG 115

Qy      70  IMKPG-LNAILGPTGGGKSSLDVLAARKDPGSLGSDVLINGAPRPN-FKCNSGYVVQD 127
      : | : | : | : | : | : | | | | | | | | : | : | : |
Db     116  ETRDGEIMAVLGASGSGKSTLIDALANRIAGSLKGTVKLNGETLQSRMLKVISAYVMQD 175

Qy     128  DVMVGTLTVRENLFQSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGTQFIRGVS 187
      | : : | | | | | : | | | : : | : | : | : | : | : | : | : |
Db     176  DLLFPMLTVEETLMAFAEFLRPSLPKSKKKLRVQALIDQLGIRNAAKTIIGDEGHRGIS 235

Qy     188  GGERKRTSIGMELITDPSILFLDEPTTGLDSSSTANAVLLLLKRMKSQGRTIIFSIIHQPRY 247
      | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db     236  GGERRRVSIGIDIHDPILLFLDEPTSLGSDTSAFMVVKVKRIAQSGSIVIMSIHQPSH 295

Qy     248  SIFKLFDSTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDII-----NG 300
      : | | | : | | : | : | : | : | : | : | : | : | |
Db     296  RVLGLLDRLIFLSRGHTIVYSGSPASLRPFTEFGSPIPENENRTEFALDLIRELEGSAGG 355

Qy     301  DSTAVALNREEDFKATEIIPEPSKQDKPLIEKLAIEIVNSSFYKETKAELHQ---LSGGEK 357
      : | : | | : : | : | | : | | : | : | : | : | : | |
Db     356  TRGLIEFNK----KWQEMKKQSNRQPPLTPP-SSYPNLTILKEAIAASIRGKLVSGGES 410

Qy     358  -----KKKITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIIVTVVLGLVIGA 411
      | | | | | | : : : | | | | | : | : | : | : | : | : |
Db     411  VAHGGATTNTTLLAVPAFANPMWIEIKTLSKRSMNLNRRQPELFGRIASVVTGFIAT 470

Qy     412  IYFGLKNDSTGIQNRAGVLFLLTTNQCFSSVSAVELFVVEKKLFIHEYISGYRVSSYFL 471
      : : | | | : | | | | : : : | : : | : : | : | | | |
Db     471  VFWRLDNSPKGVQERLGFFAFAMSTMFTCADALPVFLQERYIFMRETAYNAYRRSSYVL 530

Qy     472  GKLLSDLLPMTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQ 531
      : | : | : | | : : | | : : : | | | : :
Db     531  SHAIVS-FPSLIFLSVAFAATTYWAVGLDGLTGLLFYCLIIILASFSWSSGSFVTFLSGVV 589

Qy     532  SVVSVAATLLMTICFVMMIFSGLLVNLTTIASWSLWQYFSPRYGFTALQHNEFLGQNF 591
      : : | : : : : | : | : | : | : | : | : | : | : |
Db     590  PSVMLGYTIIVVAILAYLLFSGFFINRNPIDYWIWEHYMSLVKYPYEAVLQNEFSDATK 649

Qy     592  C--PGLNATGNPN-----CNYATC--TGEEYLVKQG-IDLSP 623
      | | : | | : | | | : | : | : | : |

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Db 650 CFVRGVQIFDNTPLGELPEVMKLLKLTGTVSKSLGVTISSTTCLTTGSDILRQGVVQLSK 709

Qy 624 WGLWKNHVALACMIVIFLTIA---YLKLLF 550  
| :|:|:| : :|:|

Db 710 WN-----CLFITVAFGFFFRILF 727

# RESULT 15

E96742

probable ABC transporter F17M19.11 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: E96742

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C. Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L. J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E96742

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-609 <STO>

A;Cross-references: UNIPROT:Q9C8W6; UNIPARC:UPI000009EF81; GB:AE005173; NID:g6978921; PIDN:AAF34313.1; GSPDB:GN00141

C;Genetics:

A;Gene: F17M19.11

A;Map position: 1

C;Superfamily: fruit fly white protein; ATP-binding cassette homology

Query Match 21.3%; Score 712.5; DB 2; Length 609;  
Best Local Similarity 31.0%; Pred. No. 3.6e-42;  
Matches 190; Conservative 125; Mismatches 256; Indels 41; Gaps 16;

Qy 56 RKPVEKEILSNINGIMKPG-LNAILGPTGGGKSSLLDLVAARKDPSGLSGDVFLINGAPRP 114  
| :|:|:| :|:|:| | :|:|:| | :|:|:| :| | :|:|:|

Db 23 RSTEERTILSGVTGMISPGEFMAVLGPGSGSKSTLLNAVAGRLHGSNLTGKILINDGKIT 82

Qy 115 ANFKCNSGVYVQDDVVMGTLTVRENLFQSAALRLATMTNHEKNERINRVIQELGLDKVA 174  
:|:|:|:| :|:|:| | :|:|:| | :|:|:|

Db 83 KQTLKRIGFVAQDDLLYPHLLTVRETLVFVALLRLRPSLRTRDVKLRAAESVISELGLTKCE 142

Qy 175 DSKVGTQFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSK- 233  
: :| :|:|:|:|:|:| | :|:|:| :|:|:|:|:|:| : :| : :

Db 143 NTVVGNTFIRGISGGERKRVSAHELLINPSLVLDDEPTSGGLDATAALRLVQTLAGLAHG 202

Qy 234 QGRTIIFSIIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADF 293

